bodies in Vienna (Austria). We photographed the larvae in lateral and dorsal view immediately after capture in the field. To assess variation in body shape, we use advanced methods of geometric morphometrics.

F. König & C. Nowack

First description of a previously unnoticed intranasal gland of the Green puddle frog (*Occidozyga lima*)

In the present study we analysed the anatomy of the nasal region of Occidozyga lima (Anura, Amphibia), focussing on the glandular structures related to the olfactory system. For this purpose we investigated transverse paraffin sections of the frog's nose, stained with Petersen's azan. Normally, three major nasal glands are found in association to the anuran olfactory organs, namely the glandula nasalis medialis, the glandula nasalis lateralis and the glandula nasalis oralis interna (Gaupp, 1904). All three glands are thought to play important roles during olfaction. The glandula nasalis medialis is closely related to the vomeronasal organ, whereas the glandula nasalis lateralis opens nearby the external naris. The glandula nasalis oralis interna always occurs in conjunction with the recessus olfactorius, a rarely known additional olfactory organ of many frogs. In Occidozyga lima we were not able to find a recessus olfactorius or a glandula nasalis oralis interna. Instead, we observed a further, fourth intranasal gland, previously undescribed for the family Ranidae. This gland opens in the proximity of the external naris at the junction between the main cavity and the accessory nasal cavities. The staining pattern of this unidentified gland differs considerably from that of the lateral and medial nasal glands. Helling (1938) briefly mentioned a somewhat resembling glandular structure in two species of the family Microhylidae and in one species of the family Brevicipitidae, and called it the glandula nasalis infundibularis. If the two glands are homologue structures requires further investigation.

A. Kaliontzopoulou, V. Bandeira & M.A. Carretero

Sexual dimorphism in locomotor performance in *Podarcis* wall lizards: going multivariate

Sexual dimorphism (SD) in locomotor performance is prominent in many species of lizards. This functional pattern is related to both size and shape SD and it has been associated to sexual selection on males, related to territorial behaviour. Locomotor capacities of lacertid lizards are related to habitat variation, following ecomorphological predictions, but SD has not been extensively investigated. The few existing studies have indicated a lack of SD in this respect. We investigated SD in locomotor performance and its relation to morphological traits in a population of *Podarcis bocagei*, a species endemic to the Iberian Peninsula. We measured sprinting, climbing and clambering speed, as well as manoeuvrability, of adult male and female *P. bocagei* in a racing track. We also quantified body size and shape, including characters potentially relevant for locomotion, in the same individuals. Our results indicate that while

SD in performance is not significant when looking at each locomotor component separately, differences between sexes are significant when treating the data in a multivariate framework. This is due to differences between sexes in the trade-offs between conditions: while females are relatively stable across designs, males are fast sprinters, but suffer a visible reduction of their locomotor capacity when climbing or serpentizing. Fitting biomechanical predictions and previous observations, the morphological variables associated to locomotor performance are total body size and limb length. Our study suggests that significant, but previously unnoticed, SD may exist in locomotor performance in lacertids and remarks the importance of multivariate analyses when examining performance capacities.

A. Kosyan, M. Arakelyan & F. Danielyan

Comparison of seasonal activity and reproductions cycles of syntopic *L. agilis* and *L. strigata*

The zone of syntopy between *Lacerta agilis*, *Lacerta strigata* and *Parvilacerta parva* were discovered in vicinity of Mets Parni village, Lori Province, Armenia. 93 individuals of *L. agilis* (83.7%) and18 of *L. strigata* (16.2%) and one lizard of *P. parva* were examined during 2009-2011. According to our observations, the season activity of *L. agilis* is shorter than syntopic *L. strigata* on month. *L. strigata* emerged from hibernation at mid-April and were active until the mid-October, while *L. agilis* left winter burrows two week after *L. strigata* at the beginning of May and disappeared into hibernation on two week earlier at the end of September. Females of *L. strigata* lay thier first clutchof eggs at the end of May, whereas *L. agilis* lay the first clutch at the beginning of summer. The hatchlings of both species active till end October when the thermal conditions still favourable. Similarly, the appearance of young from winter hibernation occurs earlier than adults. Our surveys also revealed that two syntopic species possess spacial differentiation of the same slope, where in bottom of slope were met *L. strigata*, in the middle of slope were both species and on higher places near to top of slope were mainly *L. agilis*. Thus, the dates of season activity, stages of reproductive cycles as well as pattern of spacial differentiation allow to syntopic species to share resources of habitats.

M. Luznik, E.V. Buzan & B. Krystufek

Mitochondrial DNA reveals new lineage of the smooth newt Lissotriton vulgaris in SW Slovenia and Istria

The smooth newt *Lissotriton vulgaris* is represented in Slovenia by two subspecies, which differ in male epigamic traits. The nominal subspecies *L. v. vulgaris* is confined to the north-eastern part of the country, specifically to the Pannonia lowland, while the rest of the country is populated by *L. v. meridionalis*. The range borders of these two subspecies are not sharply defined because of frequent records of males displaying intermediate characters. A broad transition zone between these two subspecies is known from the rest of Europe, with some level of gene introgression. The aim of this study was to identify mitochondrial DNA (mtDNA)